

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Bartley, Timothy D.
Bogenberger, Jakob M.
Bosselman, Robert A.
Hunt, Pamela
Samal, Babru B.
- (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR STIMULATING
MEGAKARYOCYTE GROWTH AND DIFFERENTIATION
- (iii) NUMBER OF SEQUENCES: 34
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Amgen Inc.
(B) STREET: 1840 Dehavilland Drive
(C) CITY: Thousand Oaks
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 91320-1789
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/347,780
(B) FILING DATE: 30-NOV-1994
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/252,628
(B) FILING DATE: 31-MAY-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/221,768
(B) FILING DATE: 31-MAR-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/321,488
(B) FILING DATE: 12-OCT-1994
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Cook, Robert R.
(B) REGISTRATION NUMBER: 31,602
(C) REFERENCE/DOCKET NUMBER: A-290C

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Met Leu Arg Asp
1 5 10 15
Ser His Val Leu His Xaa Arg Leu Xaa Gln Xaa Pro Asp Ile Tyr
20 25 30

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

C13
cont.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Met Leu Arg Asp
1 5 10 15
Ser His Val Leu His
20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Gln Lys Glu Gln Thr Lys Ala Gln Asp Val Leu Gly Ala Val Ala
1 5 10 15
Leu

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCNCCNCCNG CNTGYGA

17

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

C13
cont. (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCARTGYAAC ACRTGNGART C

21

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp
1 5 10 15
Ser His Val Leu His
20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTACGCGTTC TAGANNNNNN T

21

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGTTTACTGA GGACTCGGAG G

21

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCGGCCGGA TAGGCCTTTT TTTTTTTTTT

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTCGGCCGGA TAGGCCTTTT TTTTTTTTTT

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCGACCTCC GAGTCCTCAG

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAGTCCTCAG TAAACTGCTT CGT

23

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGTCACGA AGCAGTTTAC

20

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cont.

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCTTTACTTC TAGGCCTG

18

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAGGTCACAA GCAGGAGGA

19

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCATAGTCC GGGACGTCG

19

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCCTCCTGCT TGTGACCTC

19

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAGGAAGGA TTCAGGGGA

19

(2) INFORMATION FOR SEQ ID NO:19:

- C13
cont.
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAACAAGTCG ACCGCCAGCC AGACACCCCG

30

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCCGGATAG GCCACTCNNN NNNT

24

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCARTGYAAN ACRTGNGART C

21

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTGGTGTGCA CTTGTG

16

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CACAAGTGCA CACCAACCCC

20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1342 base pairs

C13
cont.

(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 36..1097

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 99..1097

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 36..98

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CAGGGAGCCA CGCCAGCCAA GACACCCCGG CCAGA ATG GAG CTG ACT GAA TTG 53
Met Glu Leu Thr Glu Leu
-21 -20

CTC CTC GTG GTC ATG CTT CTC CTA ACT GCA AGG CTA ACG CTG TCC AGC 101
Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu Ser Ser
-15 -10 -5 1

CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT 149
Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg
5 10 15

GAC TCC CAT GTC CTT CAC AGC AGA CTG AGC CAG TGC CCA GAG GTT CAC 197
Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val His
20 25 30

CCT TTG CCT ACA CCT GTC CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA 245
Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly
35 40 45

GAA TGG AAA ACC CAG ATG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA 293
Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly
50 55 60 65

GCA GTG ACC CTT CTG CTG GAG GGA GTG ATG GCA GCA CGG GGA CAA CTG 341
Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu
70 75 80

GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG CAG CTT TCT GGA CAG GTC 389
Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val
85 90 95

CGT CTC CTC CTT GGG GCC CTG CAG AGC CTC CTT GGA ACC CAG CTT CCT 437
Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro
100 105 110

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cont.

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|------------|------------|------------|------------|------------|-------------|-----|-----|-----|-----|-----|-----|------------|-----|-----|-----|------|
| CCA | CAG | GGC | AGG | ACC | ACA | GCT | CAC | AAG | GAT | CCC | AAT | GCC | ATC | TTC | CTG | 485 |
| Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe | Leu | |
| 115 | | | | | | 120 | | | | 125 | | | | | | |
| AGC | TTC | CAA | CAC | CTG | CTC | CGA | GGA | AAG | GTG | CGT | TTC | CTG | ATG | CTT | GTA | 533 |
| Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu | Val | |
| 130 | | | | | | 135 | | | | 140 | | | | | 145 | |
| GGA | GGG | TCC | ACC | CTC | TGC | GTC | AGG | CGG | GCC | CCA | CCC | ACC | ACA | GCT | GTC | 581 |
| Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Arg | Ala | Pro | Pro | Thr | Thr | Ala | Val | |
| | | | | 150 | | | | | 155 | | | | | 160 | | |
| CCC | AGC | AGA | ACC | TCT | CTA | GTC | CTC | ACA | CTG | AAC | GAG | CTC | CCA | AAC | AGG | 629 |
| Pro | Ser | Arg | Thr | Ser | Leu | Val | Leu | Thr | Leu | Asn | Glu | Leu | Pro | Asn | Arg | |
| | | | 165 | | | | | 170 | | | | | 175 | | | |
| ACT | TCT | GGA | TTG | TTG | GAG | ACA | AAC | TTC | ACT | GCC | TCA | GCC | AGA | ACT | ACT | 677 |
| Thr | Ser | Gly | Leu | Leu | Glu | Thr | Asn | Phe | Thr | Ala | Ser | Ala | Arg | Thr | Thr | |
| | | 180 | | | | | 185 | | | | | 190 | | | | |
| GGC | TCT | GGG | CTT | CTG | AAG | TGG | CAG | CAG | GGA | TTC | AGA | GCC | AAG | ATT | CCT | 725 |
| Gly | Ser | Gly | Leu | Leu | Lys | Trp | Gln | Gln | Gly | Phe | Arg | Ala | Lys | Ile | Pro | |
| | 195 | | | | | 200 | | | | | 205 | | | | | |
| GGT | CTG | CTG | AAC | CAA | ACC | TCC | AGG | TCC | CTG | GAC | CAA | ATC | CCC | GGA | TAC | 773 |
| Gly | Leu | Leu | Asn | Gln | Thr | Ser | Arg | Ser | Leu | Asp | Gln | Ile | Pro | Gly | Tyr | |
| 210 | | | | | 215 | | | | | 220 | | | | | 225 | |
| CTG | AAC | AGG | ATA | CAC | GAA | CTC | TTG | AAT | GGA | ACT | CGT | GGA | CTC | TTT | CCT | 821 |
| Leu | Asn | Arg | Ile | His | Glu | Leu | Leu | Asn | Gly | Thr | Arg | Gly | Leu | Phe | Pro | |
| | | | | 230 | | | | | 235 | | | | | 240 | | |
| GGA | CCC | TCA | CGC | AGG | ACC | CTA | GGA | GCC | CCG | GAC | ATT | TCC | TCA | GGA | ACA | 869 |
| Gly | Pro | Ser | Arg | Arg | Thr | Leu | Gly | Ala | Pro | Asp | Ile | Ser | Ser | Gly | Thr | |
| | | | 245 | | | | | 250 | | | | | 255 | | | |
| TCA | GAC | ACA | GGC | TCC | CTG | CCA | CCC | AAC | CTC | CAG | CCT | GGA | TAT | TCT | CCT | 917 |
| Ser | Asp | Thr | Gly | Ser | Leu | Pro | Pro | Asn | Leu | Gln | Pro | Gly | Tyr | Ser | Pro | |
| | | 260 | | | | | 265 | | | | | 270 | | | | |
| TCC | CCA | ACC | CAT | CCT | CCT | ACT | GGA | CAG | TAT | ACG | CTC | TTC | CCT | CTT | CCA | 965 |
| Ser | Pro | Thr | His | Pro | Pro | Thr | Gly | Gln | Tyr | Thr | Leu | Phe | Pro | Leu | Pro | |
| | 275 | | | | | 280 | | | | | 285 | | | | | |
| CCC | ACC | TTG | CCC | ACC | CCT | GTG | GTC | CAG | CTC | CAC | CCC | CTG | CTT | CCT | GAC | 1013 |
| Pro | Thr | Leu | Pro | Thr | Pro | Val | Val | Gln | Leu | His | Pro | Leu | Leu | Pro | Asp | |
| 290 | | | | | 295 | | | | | 300 | | | | | 305 | |
| CCT | TCT | GCT | CCA | ACG | CCC | ACC | CCT | ACC | AGC | CCT | CTT | CTA | AAC | ACA | TCC | 1061 |
| Pro | Ser | Ala | Pro | Thr | Pro | Thr | Pro | Thr | Ser | Pro | Leu | Leu | Asn | Thr | Ser | |
| | | | | 310 | | | | | 315 | | | | | 320 | | |
| TAC | ACC | CAC | TCC | CAG | AAT | CTG | TCT | CAG | GAA | GGG | TAA | GGTTCTCAGA | | | | 1107 |
| Tyr | Thr | His | Ser | Gln | Asn | Leu | Ser | Gln | Glu | Gly | * | | | | | |
| | | | 325 | | | | | 330 | | | | | | | | |
| CACTGCCGAC | ATCAGCATTG | TCTCGTGTAC | AGCTCCCTTC | CCTGCAGGGC | GCCCCCTGGGA | | | | | | | | | | | 1167 |

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cont.

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|---|------|
| GACAACTGGA CAAGATTTCC TACTTTCTCC TGAAACCCAA AGCCCTGGTA AAAGGGATAC | 1227 |
| ACAGGACTGA AAAGGGAATC ATTTTTCAC TACATTATA AACCTTCAGA AGCTATTTTTT | 1287 |
| TTAAGCTATC AGCAATACTC ATCAGAGCAG CTAGCTCTTT GGTCTATTTT CTGCA | 1342 |

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala
-21 -20 -15 -10

Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val
-5 1 5 10

Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser
15 20 25

Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala
30 35 40

Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys
45 50 55

Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
60 65 70 75

Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly
80 85 90

Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu
95 100 105

Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp
110 115 120

Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val
125 130 135

Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala
140 145 150 155

Pro Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu
160 165 170

Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr
175 180 185

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Ala Ser Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly
190 195 200

Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu
205 210 215

Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn Gly
220 225 230 235

Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro
240 245 250

Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu
255 260 265

Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr
270 275 280

Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu
285 290 295

His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser
300 305 310 315

Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu
320 325 330

Gly *

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 97..891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

| | |
|---|-----|
| AGGGAGCCAC GCCAGCCAGA CACCCCGGCC AGAATGGAGC TGA | 60 |
| CTGCTGCTTC TCCTAACTGC AAGGCTAACG CTGTCC AGC CCG GCT CCT CCT GCT | 114 |
| Ser Pro Ala Pro Pro Ala | |
| 1 5 | |
| TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT GAC TCC CAT GTC CTT | 162 |
| Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu | |
| 10 15 20 | |

C13
cont.

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CAC | AGC | AGA | CTG | AGC | CAG | TGC | CCA | GAG | GTT | CAC | CCT | TTG | CCT | ACA | CCT | 210 |
| His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val | His | Pro | Leu | Pro | Thr | Pro | |
| | 25 | | | | | | 30 | | | | | 35 | | | | |
| GTC | CTG | CTG | CCT | GCT | GTG | GAC | TTT | AGC | TTG | GGA | GAA | TGG | AAA | ACC | CAG | 258 |
| Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu | Gly | Glu | Trp | Lys | Thr | Gln | |
| | 40 | | | | | 45 | | | | | 50 | | | | | |
| ATG | GAG | GAG | ACC | AAG | GCA | CAG | GAC | ATT | CTG | GGA | GCA | GTG | ACC | CTT | CTG | 306 |
| Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu | Gly | Ala | Val | Thr | Leu | Leu | |
| 55 | | | | | 60 | | | | | 65 | | | | | 70 | |
| CTG | GAG | GGA | GTG | ATG | GCA | GCA | CGG | GGA | CAA | CTG | GGA | CCC | ACT | TGC | CTC | 354 |
| Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln | Leu | Gly | Pro | Thr | Cys | Leu | |
| | | | | 75 | | | | | 80 | | | | | 85 | | |
| TCA | TCC | CTC | CTG | GGG | CAG | CTT | TCT | GGA | CAG | GTC | CGT | CTC | CTC | CTT | GGG | 402 |
| Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln | Val | Arg | Leu | Leu | Leu | Gly | |
| | | | 90 | | | | | 95 | | | | | 100 | | | |
| GCC | CTG | CAG | AGC | CTC | CTT | GGA | ACC | CAG | CTT | CCT | CCA | CAG | GGC | AGG | ACC | 450 |
| Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu | Pro | Pro | Gln | Gly | Arg | Thr | |
| | | 105 | | | | | 110 | | | | | 115 | | | | |
| ACA | GCT | CAC | AAG | GAT | CCC | AAT | GCC | ATC | TTC | CTG | AGC | TTC | CAA | CAC | CTG | 498 |
| Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe | Leu | Ser | Phe | Gln | His | Leu | |
| | 120 | | | | | 125 | | | | | 130 | | | | | |
| CTC | CGA | GGA | AAG | GAC | TTC | TGG | ATT | GTT | GGA | GAC | AAA | CTT | CAC | TGC | CTC | 546 |
| Leu | Arg | Gly | Lys | Asp | Phe | Trp | Ile | Val | Gly | Asp | Lys | Leu | His | Cys | Leu | |
| 135 | | | | | 140 | | | | | 145 | | | | | 150 | |
| AGC | CAG | AAC | TAC | TGG | CTC | TGG | GCT | TCT | GAA | GTG | GCA | GCA | GGG | ATT | CAG | 594 |
| Ser | Gln | Asn | Tyr | Trp | Leu | Trp | Ala | Ser | Glu | Val | Ala | Ala | Gly | Ile | Gln | |
| | | | | 155 | | | | | 160 | | | | | 165 | | |
| AGC | CAA | GAT | TCC | TGG | TCT | GCT | GAA | CCA | AAC | CTC | CAG | GTC | CCT | GGA | CCA | 642 |
| Ser | Gln | Asp | Ser | Trp | Ser | Ala | Glu | Pro | Asn | Leu | Gln | Val | Pro | Gly | Pro | |
| | | | 170 | | | | | 175 | | | | | 180 | | | |
| AAT | CCC | CGG | ATA | CCT | GAA | CAG | GAT | ACA | CGA | ACT | CTT | GAA | TGG | AAC | TCG | 690 |
| Asn | Pro | Arg | Ile | Pro | Glu | Gln | Asp | Thr | Arg | Thr | Leu | Glu | Trp | Asn | Ser | |
| | | 185 | | | | | 190 | | | | | 195 | | | | |
| TGG | ACT | CTT | TCC | TGG | ACC | CTC | ACG | CAG | GAC | CCT | AGG | AGC | CCC | GGA | CAT | 738 |
| Trp | Thr | Leu | Ser | Trp | Thr | Leu | Thr | Gln | Asp | Pro | Arg | Ser | Pro | Gly | His | |
| | 200 | | | | | 205 | | | | | 210 | | | | | |
| TTC | CTC | AGG | AAC | ATC | AGA | CAC | AGG | CTC | CCT | GCC | ACC | CAA | CCT | CCA | GCC | 786 |
| Phe | Leu | Arg | Asn | Ile | Arg | His | Arg | Leu | Pro | Ala | Thr | Gln | Pro | Pro | Ala | |
| 215 | | | | | 220 | | | | | 225 | | | | | 230 | |
| TGG | ATA | TTC | TCC | TTC | CCC | AAC | CCA | TCC | TCC | TAC | TGG | ACA | GTA | TAC | GCT | 834 |
| Trp | Ile | Phe | Ser | Phe | Pro | Asn | Pro | Ser | Ser | Tyr | Trp | Thr | Val | Tyr | Ala | |
| | | | | 235 | | | | | 240 | | | | | 245 | | |

C13
cont.

| | |
|--|------|
| CTT CCC TCT TCC ACC CAC CTT GCC CAC CCC TGT GGT CCA GCT CCA CCC | 882 |
| Leu Pro Ser Ser Thr His Leu Ala His Pro Cys Gly Pro Ala Pro Pro | |
| 250 255 260 | |
| CCT GCT TCC TGACCCTTCT GCTCCAACGC CCACCCCTAC CAGCCCTCTT | 931 |
| Pro Ala Ser | |
| 265 | |
| CTAAACACAT CCTACACCCA CTCCCAGAAT CTGTCTCAGG AAGGGTAAGG TTCTCAGACA | 991 |
| CTGCCGACAT CAGCATTGTC TCGTGTACAG CTCCCTTCCC TGCAGGGCGC CCCTGGGAGA | 1051 |
| CAACTGGACA AGATTTCTCTA CTTTCTCCTG AAACCCAAAG CCCTGGTAAA AGGGATACAC | 1111 |
| AGGACTGAAA AGGGAATCAT TTTTCACTGT ACATTATAAA CCTTCAGAAG CTA | 1164 |

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

C13
cont.

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln |
| | 65 | | | | 70 | | | | 75 | | | | | 80 | |
| Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln |
| | | | | 85 | | | | 90 | | | | | | 95 | |
| Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu |
| | | 100 | | | | | 105 | | | | | | 110 | | |
| Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Asp | Phe | Trp | Ile | Val | Gly |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Asp | Lys | Leu | His | Cys | Leu | Ser | Gln | Asn | Tyr | Trp | Leu | Trp | Ala | Ser | Glu |
| 145 | | | | | 150 | | | | 155 | | | | | | 160 |

Val Ala Ala Gly Ile Gln Ser Gln Asp Ser Trp Ser Ala Glu Pro Asn
165 170 175

Leu Gln Val Pro Gly Pro Asn Pro Arg Ile Pro Glu Gln Asp Thr Arg
180 185 190

Thr Leu Glu Trp Asn Ser Trp Thr Leu Ser Trp Thr Leu Thr Gln Asp
195 200 205

Pro Arg Ser Pro Gly His Phe Leu Arg Asn Ile Arg His Arg Leu Pro
210 215 220

Ala Thr Gln Pro Pro Ala Trp Ile Phe Ser Phe Pro Asn Pro Ser Ser
225 230 235 240

Tyr Trp Thr Val Tyr Ala Leu Pro Ser Ser Thr His Leu Ala His Pro
245 250 255

Cys Gly Pro Ala Pro Pro Pro Ala Ser
260 265

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 498 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..498

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 7..498

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 1..6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | |
|---|-----|
| ATG AAA AGT CCT GCA CCA CCT GCA TGT GAT TTA CGG GTC CTG TCT AAA | 48 |
| Met Lys Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys | |
| -2 1 5 10 | |
| CTG CTG CGC GAC TCT CAC GTG CTG CAC TCT CGT CTG TCC CAG TGC CCG | 96 |
| Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro | |
| 15 20 25 30 | |
| GAA GTT CAC CCG CTG CCG ACC CCG GTT CTG CTT CCG GCT GTC GAC TTC | 144 |
| Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe | |
| 35 40 45 | |

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C13
cont.

| | |
|---|-----|
| TCC CTG GGT GAA TGG AAA ACC CAG ATG GAA GAG ACC AAA GCT CAG GAC | 192 |
| Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp | |
| 50 55 60 | |
| ATC CTG GGT GCA GTA ACT CTG CTT CTG GAA GGC GTT ATG GCT GCA CGT | 240 |
| Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg | |
| 65 70 75 | |
| GGC CAG CTT GGC CCG ACC TGC CTG TCT TCC CTG CTT GGC CAG CTG TCT | 288 |
| Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser | |
| 80 85 90 | |
| GGC CAG GTT CGT CTG CTG CTC GGC GCT CTG CAG TCT CTG CTT GGC ACC | 336 |
| Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr | |
| 95 100 105 110 | |
| CAG CTG CCG CCA CAG GGC CGT ACC ACT GCT CAC AAG GAT CCG AAC GCT | 384 |
| Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala | |
| 115 120 125 | |
| ATC TTC CTG TCT TTC CAG CAC CTG CTG CGT GGC AAA GTT CGT TTC CTG | 432 |
| Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu | |
| 130 135 140 | |
| ATG CTG GTT GGC GGT TCT ACC CTG TGC GTT CGT CGG GCG CCG CCA ACC | 480 |
| Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr | |
| 145 150 155 | |
| ACT GCT GTT CCG TCT TAA | 498 |
| Thr Ala Val Pro Ser * | |
| 160 | |

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

| | |
|---|--|
| Met Lys Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys | |
| -2 1 5 10 | |
| Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro | |
| 15 20 25 30 | |
| Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe | |
| 35 40 45 | |
| Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp | |
| 50 55 60 | |

Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg
65 70 75
Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser
80 85 90
Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr
95 100 105 110
Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala
115 120 125
Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu
130 135 140
Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr
145 150 155
Thr Ala Val Pro Ser *

160

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAGCTCACTA GTGTCGACCT GCAG

24

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTGCAGGTCG AACTAGTGA GCTC

24

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:

C13
cont.

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCATAATTT TTAAAAAATT CATTTGACAA ATGCTAAAAT TCTTGATTAA TATTCTCAAT 60
TGTGAGCGCT CACAATTTAT 80

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

C¹³
cond.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGATAAATTG TGAGCGCTCA CAATTGAGAA TATTAATCAA GAATTTTAGC ATTTGTCAAA 60
TGAATTTTTT AAAAATTATG AGACGT 86

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GACGTCTCAT AATTTTTTAAA AAATTCATTT GACAAATGCT AAAATTCCTG ATTAATATTC 60
TCAATTGTGA GCGCTCACAA TTTATCGAT 89